more binding domains of Gux1, one or more catalytic domains of a glycoside hydrolase other than Gux1, one or more binding domains of a glycoside hydrolase other than Gux1, or any combination thereof. Further examples include immunoglobulin molecules and portions thereof, peptide tags such as histidine tag (6-His) (SEQ ID NO: 8), leucine zipper, substrate targeting moieties, signal peptides, and the like. Fusion proteins are also meant to encompass variants and derivatives of Gux1 polypeptides that are generated by conventional site-directed mutagenesis and more modern techniques such as directed evolution, discussed infra.

C1

Please delete the paragraph on page 20, lines 4-10, and replace it with the following paragraph:

Gux1 polypeptides can be fused to heterologous polypeptides to facilitate purification. Many available heterologous peptides (peptide tags) allow selective binding of the fusion protein to a binding partner. Non-limiting examples of peptide tags include 6-His (SEQ ID NO: 8), thioredoxin, hemaglutinin, GST, and the OmpA signal sequence tag. A binding partner that recognizes and binds to the heterologous peptide can be any molecule or compound, including metal ions (for example, metal affinity columns), antibodies, antibody fragments, or any protein or peptide that preferentially binds the heterologous peptide to permit purification of the fusion protein.

C2

Please delete the table on page 33, and replace it with the following table:

Table 3. Multiple amino acid sequence alignment of a Gux1 first catalytic domain and polypeptides with Glycoside Hydrolase Family 48 catalytic domains.

Multialignment of related Glycoside Hydrolase Family 48 catalytic domain
GH48_Ace: *Acidothermus cellulolyticus* Gux1 catalytic domain GH48 (SEQ ID NO: 9)
GuxB_Cfi: Cellulomonas fimi CBHB(beta-1,4-exocellobiohydrolase). GeneBank Acc. # AAB00822 (SEQ ID NO: 10)
E6_Tfu: Thermobifida fusca E6 (beta-1,4-exocellulase). GeneBank Acc. # AF144563 (SEQ ID NO: 11)

```
GH48_Ace        PYIQRFLTMYNKIHDPANGYFSPQG---IPYHSVETLIVEAPDYGHETTSEAYSFWLWLEATY (SEQ ID NO:9)
GuxB_Cfi        EYAQRFLAQYDKIKDPANGYFSAQG---IPYHAVETLMVEAPDYGHETTSEAYSYWLWLEALY (SEQ ID NO:10)
E6_Tfu          SYDQAFLEQYEKIKDPASGYFREFNGLLVPYHSVETMIVEAPDHGHQTTSEAFSYYLWLEAYY (SEQ ID NO:11)
                 * * **  *:**:***.***   .   :***:***::*****:**:*****:*::***** *

GH48_Ace        GAVTGNWTPFNNAWTTMETYMIPQHADQPNNASYNPNSPASYAPEEPLPSMYPVAIDSSV
GuxB_Cfi        GQVTQDWAPLNHAWDTMEKYMIPQSVDQPTNSFYNPNSPATYAPEFNHPSSYPSQLNSGI
E6_Tfu          GRVTGDWKPLHDAWESMETFIIPGTKDQPTNSAYNPNSPATYIPEQPNADGYPSPLMNNV
                * ** :* *::.** :**.::**   ***.*: *******:* **   .. **  : ..:

GH48_Ace        PVGHDPLAAELQSTYGTPDIYGMHWLADVDNIYGYGDSPGGGCELGPSAKGVSYINTFQR
GuxB_Cfi        SGGTDPIGAELKATYGNADVYQMHWLADVDNIYGFGATPGAGCTLGPTATGTSFINTFQR
E6_Tfu          PVGQDPLAQELSSTYGTNEIYGMHWLLDVDNVYGFGFCGDG------TDDAPAYINTYQR
                . * **:. **.:***. ::* **** ****:**:*   ..      :  . ::****:**

GH48_Ace        GSQESVWETVTQPTCDNGKYGGAHGYVDLFIQG-STPPQWKYTDAPDADARAVQAAYWAY
GuxB_Cfi        GPQESVWETVPQPSCEEFKYGGKNGYLDLFTKDASYAKQWKYTSASDADARAVEAVYWAN
E6_Tfu          GARESVWETIPHPSCDDFTHGGPNGYLDLFTDDQNYAKQWRYTNAPDADARAVQVMFWAH
                *.:******:.:*:*:: .:** :**:*** .. . . **:**.*.*******:. :**

GH48_Ace        TWASAQGKASAIAPTIAKASQTGDYLRYSLFDKYFKQVGNCYPASSCPGATGRQSETYLI
GuxB_Cfi        QWATEQGKAADVAATVAKAAKMGDYLRYTLFDKYFKKIG--CTSPTCAAGQGREAAHYLL
E6_Tfu          EWAKEQGKENEIAGLMDKASKMGDYLRYAMFDKYFKKIGNCVGATSCPGGQGKDSAHYLL
                 **. ***   :*  : **:: ******::******::*    :.:*... *:::  **:

GH48_Ace        GWYYAWGGS---SQGWAWRIGDGAAHFGYQNPLAAWAMSNVTPLIPLSPTAKSDWAASLQ
GuxB_Cfi        SWYMAWGGATDTSSGWAWRIGSSHAHFGYQNPLAAWALSTDPKLTPKSPTAKADWAASMQ
E6_Tfu          SWYYSWGGSLDTSSAWAWRIGSSSSHQGYQNVLAAYALSQVPELQPDSPTGVQDWATSFD
                .** :***:   *..******.. :* **** ***:*:*  . * * ***.  ***:*::

GH48_Ace        RQLEFYQWLQSAEGAIAGGATNSWNGNYGTPPAGDSTFYGMAYDWEPVYHDPPSNNWFGF
GuxB_Cfi        RQLEFYTWLQASNGGIAGGATNSWDGAYAQPPAGTPTFYGMGYTEAPVYVDPPSNRWFGM
E6_Tfu          RQLEFLQWLQSAEGGIAGGATNSWKGSYDTPPTGLSQFYGMYYDWQPVWNDPPSNNWFGF
                ***** ***:::*.*********.* *  **:* . **** *   **: *****.***:

GH48_Ace        QAWSMERVAEYYYVTGDPKAKALLDKWVAWVKPNVTTG-----ASWSIPSNLSWSGQPDT
GuxB_Cfi        QAWGVQRVAELYYASGNAQAKKILDKWVPWVVANISTDG----ASWKVPSELKWTGKPDT
E6_Tfu          QVWNMERVAQLYYVTGDARAEAILDKWVPWAIQHTDVDADNGGQNFQVPSDLEWSGQPDT
                *.*.::***: **.:*:.:*: :*****.*.  :  ..       .:.:**:*.*:*:***

GH48_Ace        WNPSNPGTNANLHVTITSSGQDVGVAAALAKTLEYYAAKSGDTASRDLAKGLLDSMWNND
GuxB_Cfi        WNAAAPTGNPGLTVEVTSYGQDVGVAADTARALLFYAAKSGDTASRDKAKALLDAIWANN
E6_Tfu          WTG-TYTGNPNLHVQVVSYSQDVGVTAALAKTLMYYAKRSGDTTALATAEGLLDALLAHR
                *.      *..* * :.* .*****:*  *::* :** :****::   *:.***::  :

GH48_Ace        QDSLGVSTPETRTDYSRFTQVYDPTTGDGLYIPSGWTGTMPNGDQIKPGATFLSIRSWYT
GuxB_Cfi        QDPLGVSAVETRGDYKRFDDTYVAN-GDGIYIPSGWTGTMPNGDVIKPGVSFLDIRSFYK
E6_Tfu          -DSIGIATPEQ-PSWDRLDDPWDGS--EGLYVPPGWSGTMPNGDRIEPGATFLSIRSFYK
                 *.:*::: *   .:.*: : :  .  :*:*:*.**:******* *:**.:**.***:*.

GH48_Ace        KDPQWSKVQAYLNGG---PAPTFNYHRFWAESDFAMANADFGMLFPSGSP
GuxB_Cfi        KDPNWSKVQTFLDGG---AEPQFRYHRFWAQTAVAGALADYARLFDDGTT
E6_Tfu          NDPLWPQVEAHLNDPQNVPAPIVERHRFWAQVEIATAFAAHDELFGAGAP
                :** *.:*::.*:.    . * .. *****:  .* * * .  **  *:.
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C3